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## SEQUENCE LISTING

&lt;110&gt; CHUGAI SEIYAKU KABUSHIKI KAISHA

OZAKI Shuji

ABE Masahiro

&lt;120&gt; Cell Death-Inducing Agent

&lt;130&gt; C1-A0220P

&lt;140&gt; PCT/JP03/13063

&lt;141&gt; 2003-10-10

&lt;150&gt; JP 2002-299289

&lt;151&gt; 2002-10-11

&lt;160&gt; 14

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

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&lt;221&gt; CDS

&lt;222&gt; (103).. (546)

&lt;400&gt; 1

tacgactcac tatagggcaa gcagtggat caacgcagag tacgcgggga atctatgatc 60

agtgtcctct ctacacagtc cctgacgaca ctgactccaa cc atg cga tgg agc 114

Met Arg Trp Ser

1

tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt gtc cat tgc cag 162

Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly Val His Cys Gln

5

10

15

20

gtc cag ttg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 210

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser

25

30

35

gtg aag atg tct tgt aag gct tct ggc tac acc ttc aca gac tac ttt 258

Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe

40

45

50

ata cac tgg gtg aaa cag agg cct gga cag gga ctt gaa tgg att gga 306

Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly

55

60

65

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tgg att ttt cct gga gat gat act act gat tac aat gag aag ttc agg 354

Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg

70

75

80

ggc aag acc aca ctg act gca gac aaa tcc tcc agc aca gcc tac att 402

Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile

85

90

95

100

ttg ctc agc agc ctg acc tct gag gac tct gcg atg tat ttc tgt gta 450

Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val

105

110

115

agg agt gac gac ttt gac tac tgg ggc gag ggc acc act ctc aca gtc 498

Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val

120

125

130

tcc tca gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct gct g 547

Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Ala

135

140

145

&lt;210&gt; 2

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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&lt;400&gt; 2

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly  
1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn  
65 70 75 80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met  
100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr  
115 120 125

Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro

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130

135

140

Leu Ala Pro Ala

145

&lt;210&gt; 3

&lt;211&gt; 535

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (103).. (534)

&lt;400&gt; 3

ctaatacgac tcactatagg gcaagcagtg gtatcaacgc agagtacgcg gggactwatg 60

agaatagcag taattagcta gggaccaaaa ttcaaagaca aa atg cat ttt caa 114

Met His Phe Gln

1

gtg cag att ttc agc ttc ctg cta atc agt gcc tca gtc atc atg tcc 162

Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser

5

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15

20

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aga gga caa att gtt ctc acc cag tgc cca gca atc atg tct gca tct 210

Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser

25

30

35

cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt gta agt 258

Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser

40

45

50

tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa ctc tgg 306

Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp

55

60

65

att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc ttc agt 354

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser

70

75

80

ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga atg gag 402

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu

85

90

95

100

gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt tat cca 450

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro

105

110

115

ccc acg ttc ggc tgc ggg aca aag ttg gag ata aaa cgg gct gat gct 498

Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala

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120

125

130

gca cca act gta tcc atc ttc cca cca tcc agt gag c

535

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu

135

140

&lt;210&gt; 4

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 4

Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

1

5

10

15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile

20

25

30

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

35

40

45

Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe

50

55

60

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro

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65                                      70                                      75                                      80

Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile

85                                      90                                      95

Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg

100                                      105                                      110

Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys

115                                      120                                      125

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu

130                                      135                                      140

&lt;210&gt; 5

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14).. (775)

<223> Description of Artificial Sequence:an artificially  
synthesized DNA sequence



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&lt;400&gt; 5

cctgaattcc acc atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca 49

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser

1

5

10

ata act gca ggt gtc cat tgc cag gtc cag ttg cag cag tct gga cct 97

Ile Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro

15

20

25

gag ctg gtg aag cct ggg gct tca gtg aag atg tct tgt aag gct tct 145

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser

30

35

40

ggc tac acc ttc aca gac tac ttt ata cac tgg gtg aaa cag agg cct 193

Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro

45

50

55

60

gga cag gga ctt gaa tgg att gga tgg att ttt cct gga gat gat act 241

Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr

65

70

75

act gat tac aat gag aag ttc agg ggc aag acc aca ctg act gca gac 289

Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp

80

85

90

aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag 337

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Lys Ser Ser Ser Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu

95

100

105

gac tct gcg atg tat ttc tgt gta agg agt gac gac ttt gac tac tgg 385

Asp Ser Ala Met Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp

110

115

120

ggc cag ggc acc act ctc aca gtc tcc tca ggt gga ggc ggt agc caa 433

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gln

125

130

135

140

att gtt ctc acc cag tcg cca gca atc atg tct gca tct cca ggg gag 481

Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu

145

150

155

aag gtc acc ata acc tgc agt gcc agc tca agt gta agt tac atg cac 529

Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His

160

165

170

tgg ttc cag cag aag cca ggc act ttt ccc aaa ctc tgg att tat agc 577

Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser

175

180

185

aca tcc aac ctg gct tct gga gtc cct act cgc ttc agt ggc agt gga 625

Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly

190

195

200

. 1 1 / 1 7

tct ggg acc tct tac tct ctc aca atc agc cga atg gag gct gaa gat 673  
Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp  
205 210 215 220

gct gcc act tat tac tgc cag caa agg acg agt tat cca ccc acg ttc 721  
Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe  
225 230 235

ggc tcg ggg aca aag ttg gag ata aaa gac tac aag gat gac gac gat 769  
Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp  
240 245 250

aag tga taagcggcgcg caat 789  
Lys

&lt;210&gt; 6

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: an artificially  
synthesized peptide sequence

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&lt;400&gt; 6

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly  
1 5 10 15  
Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30  
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60  
Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn  
65 70 75 80  
Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser  
85 90 95  
Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met  
100 105 110  
Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr  
115 120 125  
Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr  
130 135 140  
Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile  
145 150 155 160  
Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln  
165 170 175  
Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu  
180 185 190  
Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser

. 1 3 / 1 7

195	200	205
Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr		
210	215	220
Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr		
225	230	235
		240
Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys		
245	250	

&lt;210&gt; 7

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: an artificially  
synthesized adapter sequence

&lt;400&gt; 7

aattcccgagc acagtggtag ataagtaag

29

&lt;210&gt; 8

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized adapter sequence

&lt;400&gt; 8

tcgacttact tatctaccac'tgtgctggg

29

&lt;210&gt; 9

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

&lt;400&gt; 9

caggggccag tggatagact gatg

24

&lt;210&gt; 10

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

&lt;400&gt; 10

gotcactgga tggtaggaag atg

23

&lt;210&gt; 11

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

&lt;400&gt; 11

cctgaattcc accatgcgat ggagctggat ctttc

35

&lt;210&gt; 12

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 12

aatttggtta ccgcctccac ctgaggagac tgtgagagtg gtgccct

47

<210> 13

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 13

tcctcaggtg gaggcggtag ccaaattggt ctcacccagt cgccagc

47

<210> 14

<211> 68

<212> DNA

<213> Artificial Sequence



. 1 7 / 1 7

&lt;220&gt;

<223> Description of Artificial Sequence: an artificially  
synthesized primer sequence

&lt;400&gt; 14

attgcggccg cttatcactt atcgtcgtca tccctgtagt cttttatctc caactttgtc 60  
cccgagcc 68